



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/988,067A  
Source: OIP  
Date Processed by STIC: 11/13/02

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



**Does Not Comply**  
**Corrected Diskette Needed**

**OIPE**

**RAW SEQUENCE LISTING**

DATE: 11/13/2002

PATENT APPLICATION: US/09/988,067A

TIME: 14:03:29

Input Set : A:\06132.040002.SEQLIST.TXT

Output Set: N:\CRF4\11132002\I988067A.raw

4 <110> APPLICANT: Haas, Rainer  
5 Kleanthous, Harold  
6 Tomb, Jean-Francois  
7 Miller, Charles  
8 Al-Garawi, Amal  
9 Odenbreit, Stefan  
10 Meyer, Thomas  
14 <120> TITLE OF INVENTION: Helicobacter Polypeptides and  
15 Corresponding Polynucleotide Molecules  
18 <130> FILE REFERENCE: 06132/040002  
20 <140> CURRENT APPLICATION NUMBER: US 09/988,067A  
21 <141> CURRENT FILING DATE: 2001-11-16  
23 <150> PRIOR APPLICATION NUMBER: US 08/831,309  
24 <151> PRIOR FILING DATE: 1997-04-01  
26 <160> NUMBER OF SEQ ID NOS: 112  
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0

**ERRORED SEQUENCES**

*See p.5 for explanation of errors*

2540 <210> SEQ ID NO: 34  
2541 <211> LENGTH: 385  
2542 <212> TYPE: PRT  
2543 <213> ORGANISM: Helicobacter pylori  
2545 <400> SEQUENCE: 34  
2546 Met Glu Ser Val Lys Thr Gly Lys Thr Asn Lys Val Gly Lys Asn Thr  
2547 1 5 10 15  
2548 Glu Met Ala Asn Thr Lys Ala Asn Lys Glu Ala His Phe Lys Gln Ala  
2549 20 25 30  
2550 Ser Thr Ile Thr Asn Ile Ile Arg Ser Ile Arg Gly Ile Phe Thr Lys  
2551 35 40 45  
2552 Ile Ala Lys Lys Val Arg Gly Leu Val Lys Lys His Pro Lys Lys Ser  
2553 50 55 60  
2554 Ser Ala Ala Leu Val Val Leu Thr His Ile Ala Cys Lys Lys Ala Lys  
2555 65 70 75 80  
2556 Glu Leu Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu  
2557 85 90 95  
2558 Asn Gln Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Thr Ser  
2559 100 105 110  
2560 Leu Leu Leu Ala Ala Cys Ser Thr Gly Asp Val Ser Glu Gln Ile Glu  
2561 115 120 125  
2562 Leu Glu Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln  
2563 130 135 140

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2564 Ile Lys Val Glu Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn
2565 145 150 155 160
E--> 2566 Asn Gln Ile Lys Val Glu Gln Glu Gln Lys Thr Glu Gln Glu Xaa
2567 165 170 175
2568 Gln Lys Thr Glu Gln Glu Arg Gln Lys Thr Glu Gln Glu Lys Gln Lys
2569 180 185 190
2570 Thr Ile Lys Thr Gln Lys Asp Phe Ile Lys Tyr Val Glu Gln Asn Cys
2571 195 200 205
2572 Gln Glu Asn His Asn Gln Phe Ile Glu Lys Gly Gly Ile Lys Ala
2573 210 215 220
2574 Gly Ile Gly Ile Glu Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala
2575 225 230 235 240
2576 Lys Thr Asn Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys
2577 245 250 255
2578 Gln Pro Arg Ser Gln Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr
2579 260 265 270
2580 Leu Gln Lys Glu Leu Glu Ser Leu Pro Tyr Ser Gln Lys Ala Ile Ala
2581 275 280 285
2582 Lys Gln Val Asp Phe Tyr Arg Pro Ser Ser Ile Ala Tyr Leu Glu Leu
2583 290 295 300
2584 Asp Pro Arg Asp Phe Asn Val Thr Glu Glu Trp Gln Lys Glu Asn Leu
2585 305 310 315 320
2586 Lys Ile Arg Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Ser Leu
2587 325 330 335
2588 Lys Pro Asp Ser Gln Ala His Leu Ser Thr Ser Gln Ser Leu Leu Phe
2589 340 345 350
2590 Val Gln Lys Ile Phe Ala Asp Val Asn Lys Glu Ile Lys Val Val Ala
2591 355 360 365
2592 Asn Thr Glu Lys Lys Ala Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg
2593 370 375 380
2594 Met
2595 385
5269 <210> SEQ ID NO: 72
5270 <211> LENGTH: 581
5271 <212> TYPE: PRT
5272 <213> ORGANISM: Helicobacter pylori
5274 <400> SEQUENCE: 72
5275 Met Lys Lys Leu Val Leu Val Ile Phe Leu Thr Leu Ala Leu Ser Ile
5276 1 5 10 15
5277 Ser Ala Lys Glu Val Lys Ile Val Phe Leu Glu Thr Ser Asp Ile His
5278 20 25 30
5279 Gly Arg Leu Phe Ser Tyr Asp Tyr Ala Ile Gly Glu Gln Lys Pro Asn
5280 35 40 45
5281 Asn Gly Leu Thr Arg Ile Ala Thr Leu Ile Lys Lys Gln Arg Ala Glu
5282 50 55 60
5283 Asn Lys Asn Val Val Leu Ile Asp Ser Gly Asp Leu Leu Gln Gly Asn
5284 65 70 75 80
5285 Ser Ala Glu Leu Phe Asn Asp Glu Pro Ile His Pro Leu Val Arg Ala
5286 85 90 95

```

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```

5287 Glu Asn Asp Leu Lys Phe Asp Ile Arg Val Leu Gly Asn His Glu Phe
5288      100      105      110
5289 Asn Phe Ser Lys Asp Phe Leu Glu Lys Asn Ile Lys Gly Phe Asn Gly
5290      115      120      125
5291 Asp Val Met Asn Ala Asn Ile Ile Lys Ile Ala Asp Asn Lys Pro Phe
5292      130      135      140
5293 Val Lys Pro Tyr Ile Ile Lys Lys Ile Asp Gly Val Arg Val Ala Val
5294 145      150      155      160
5295 Val Gly Tyr Val Val Ala His Ile Pro Thr Trp Glu Ala Ser Thr Pro
5296      165      170      175
5297 Glu His Phe Ala Gly Leu Lys Phe Leu Asp Ala Glu Glu Ala Leu Lys
5298      180      185      190
5299 Lys Thr Leu Lys Glu Leu Lys Gly Lys Tyr Asp Ile Leu Ile Gly Ala
5300      195      200      205
5301 Phe His Leu Gly Arg Glu Asp Glu Lys Gly Gly Asp Gly Ile Pro Asp
5302      210      215      220
5303 Leu Ala Lys Lys Phe Pro Gln Phe Asp Ile Ile Phe Ala Gly His Glu
5304 225      230      235      240
5305 His Ala Val Tyr Asn Thr Lys Val Gly Lys Val His Thr Ile Glu Pro
5306      245      250      255
5307 Gly Ala Tyr Gly Ala Tyr Leu Ala Lys Gly Val Val Val Phe Asp Thr
5308      260      265      270
5309 Lys Thr Lys Lys Lys Ile Ile Thr Thr Glu Asn Leu Pro Thr Lys Asp
5310      275      280      285
5311 Val Pro Glu Asp Glu Glu Leu Ala Lys Lys Tyr Glu Tyr Val Asp Lys
5312      290      295      300
5313 Lys Ser Lys Glu Tyr Ala Asn Glu Val Val Gly Glu Val Thr Lys Thr
5314 305      310      315      320
5315 Phe Ile Asp Arg Pro Asp Phe Ile Thr Gly Glu Glu Lys Ile Thr Thr
5316      325      330      335
5317 Met Pro Thr Ala Ala Leu Gln Glu Thr Pro Val Ile Glu Leu Ile Asn
5318      340      345      350
5319 Lys Val Gln Lys Tyr Tyr Ala Lys Ala Asp Val Ser Ala Ala Ala Leu
5320      355      360      365
5321 Phe Asn Phe Gly Ala Asn Leu Lys Lys Gly Pro Phe Lys Arg Lys Asp
5322      370      375      380
5323 Val Thr Tyr Ile Tyr Lys Phe Ala Asn Thr Leu Ile Gly Val Arg Ile
5324 385      390      395      400
5325 Thr Gly Glu Asn Leu Leu Lys Tyr Met Glu Trp Ser Tyr Arg Phe Tyr
5326      405      410      415
5327 Asn Gln Leu Gln Pro Gly Asp Leu Thr Ile Ser Phe Asn Glu Asn Ile
5328      420      425      430
5329 Arg Gly Tyr Asn Phe Asp Met Phe Ser Gly Val Lys Tyr Gln Val Asp
5330      435      440      445
5331 Val Thr Lys Pro Ala Gly Gln Arg Ile Ile Asn Pro Thr Ile Asn Asn
5332      450      455      460
5333 Lys Pro Ile Asp Pro Lys Ala Ile Tyr Lys Leu Ala Ile Asn Asn Tyr
5334 465      470      475      480
E--> 5335 Arg Phe Gly Thr Leu Ser Thr Thr Leu Asn Leu Val Thr Asp Ala Xaa

```

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|      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 5336 |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |     |
| 5337 | Arg | Tyr | Tyr | Asn | Ser | Tyr | Asp | Glu | Leu | Gln | Asp | Asn | Gly | Gln | Ile | Arg |
| 5338 |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| 5339 | Asp | Leu | Ile | Ile | Lys | Tyr | Ile | Thr | Glu | Glu | Lys | Gly | Gly | Lys | Val | Thr |
| 5340 |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| 5341 | Pro | Glu | Leu | Glu | Gly | Asn | Trp | Glu | Ile | Ile | Asn | Tyr | Asp | Phe | Lys | Asn |
| 5342 |     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |     |
| 5343 | Pro | Leu | Leu | Glu | Lys | Leu | Arg | Glu | Lys | Leu | Lys | Glu | Gly | Ser | Ile | Lys |
| 5344 | 545 |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |     |
| 5345 | Ile | Pro | Thr | Ser | Lys | Asp | Gly | Arg | Thr | Leu | Asn | Val | Lys | Ser | Ile | Lys |
| 5346 |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     |     | 575 |     |
| 5347 | Glu | Ser | Glu | Val | Lys |     |     |     |     |     |     |     |     |     |     |     |
| 5348 |     |     |     | 580 |     |     |     |     |     |     |     |     |     |     |     |     |

## VARIABLE LOCATION SUMMARY

DATE: 11/13/2002

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Input Set : A:\06132.040002.SEQLIST.TXT

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Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in &lt;220&gt; to &lt;223&gt; section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:33; Xaa Pos. 176

Seq#:34; Xaa Pos. 176

Seq#:71; Xaa Pos. 496

Seq#:72; Xaa Pos. 496

## VERIFICATION SUMMARY

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Input Set : A:\06132.040002.SEQLIST.TXT

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L:2483 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:33  
L:2483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:584  
L:2566 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34  
L:5245 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:71  
L:5245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:1602  
L:5335 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:72